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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/898,586

DATE: 09/13/2001

TIME: 12:51:18

Input Set : A:\Cural381.app

Output Set: N:\CRF3\09132001\I898586.raw

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3 <110> APPLICANT: Gerlach, Valerie L
 4 MacDougall, John R
 5 Smithson, Glennda
 7 <120> TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
 9 <130> FILE REFERENCE: 15966-638CIP
 11 <140> CURRENT APPLICATION NUMBER: 09/898,586
 C--> 12 <141> CURRENT FILING DATE: 2001-08-27
 14 <150> PRIOR APPLICATION NUMBER: 60/177,839
 15 <151> PRIOR FILING DATE: 2000-01-25
 17 <150> PRIOR APPLICATION NUMBER: 60/176,134
 18 <151> PRIOR FILING DATE: 2000-01-14
 20 <150> PRIOR APPLICATION NUMBER: 60/175,989
 21 <151> PRIOR FILING DATE: 2000-01-13
 23 <150> PRIOR APPLICATION NUMBER: 60/218,324
 24 <151> PRIOR FILING DATE: 2000-07-14
 26 <150> PRIOR APPLICATION NUMBER: 60/220,253
 27 <151> PRIOR FILING DATE: 2000-07-24
 29 <150> PRIOR APPLICATION NUMBER: 60/178,191
 30 <151> PRIOR FILING DATE: 2000-01-26
 32 <150> PRIOR APPLICATION NUMBER: 60/178,227
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 35 <150> PRIOR APPLICATION NUMBER: 60/220,590
 36 <151> PRIOR FILING DATE: 2000-07-25
 38 <150> PRIOR APPLICATION NUMBER: 09/761,288
 39 <151> PRIOR FILING DATE: 2001-01-16
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 47 <212> TYPE: DNA
 48 <213> ORGANISM: Homo sapiens
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 53 tctttgcact ttctctgtgt ctctatttaa cagggctgtt tggaaactta ctcatcttgc 180
 54 tggccattgg ctcggtacac tgccttcaca caccatgta ttcttccct gccaatctgt 240
 55 ccttggtaga cctctgcctt ccctcagcca cagtcccca gatgctactg aacatccaaa 300
 56 cccaaaccca aaccatctcc tatcccggt gcttggtca gatgtattc tgtatgatgt 360
 57 ttgccaatat ggacaatttt ctctcacag tgaatggcata tgaccgttac gtggccatct 420
 58 gtcacccttt acattactcc accattatgg ccttgccct ctgtgcctct ctggtagctg 480
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 62 ttgtggtacc ttcagtgtgt atcctggtat cctatatcct cattgtttct gctgtgatga 720
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 64 tggtcattct tttctatgga gcaatcacag gggctctatat gagccctta tccaatcact 840
 65 ctactgaaaa agactcagcc gcatcagtc tttttatggt ttagcacct gtgttgaatc 900

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67 gaccgggcgc ggtggctcac gcctgtaatc ccagcacttt gggaggccga ggcgggtgga 1020
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81 20 25 30
83 Cys Leu Tyr Leu Thr Gly Leu Phe Gly Asn Leu Leu Ile Leu Leu Ala
84 35 40 45
86 Ile Gly Ser Asp His Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ala
87 50 55 60
89 Asn Leu Ser Leu Val Asp Leu Cys Leu Pro Ser Ala Thr Val Pro Lys
90 65 70 75 80
92 Met Leu Leu Asn Ile Gln Thr Gln Thr Gln Thr Ile Ser Tyr Pro Gly
93 85 90 95
95 Cys Leu Ala Gln Met Tyr Phe Cys Met Met Phe Ala Asn Met Asp Asn
96 100 105 110
98 Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
99 115 120 125
101 Pro Leu His Tyr Ser Thr Ile Met Ala Leu Arg Leu Cys Ala Ser Leu
102 130 135 140
104 Val Ala Ala Pro Trp Val Ile Ala Ile Leu Asn Pro Leu Leu His Thr
105 145 150 155 160
107 Leu Met Met Ala His Leu His Phe Cys Ser Asp Asn Val Ile His His
108 165 170 175
110 Phe Phe Cys Asp Ile Asn Ser Leu Leu Pro Leu Ser Cys Ser Asp Thr
111 180 185 190
113 Ser Leu Asn Gln Leu Ser Val Leu Ala Thr Val Gly Leu Ile Phe Val
114 195 200 205
116 Val Pro Ser Val Cys Ile Leu Val Ser Tyr Ile Leu Ile Val Ser Ala
117 210 215 220
119 Val Met Lys Val Pro Ser Ala Gln Gly Lys Leu Lys Ala Phe Ser Thr
120 225 230 235 240
122 Cys Gly Ser His Leu Ala Leu Val Ile Leu Phe Tyr Gly Ala Ile Thr
123 245 250 255
125 Gly Val Tyr Met Ser Pro Leu Ser Asn His Ser Thr Glu Lys Asp Ser
126 260 265 270
128 Ala Ala Ser Val Ile Phe Met Val Val Ala Pro Val Leu Asn Pro Phe
129 275 280 285
131 Ile Tyr Ser Leu Arg Asn Asn Glu Leu Lys Gly Thr Leu Lys Lys Thr
132 290 295 300
134 Leu Ser Arg Pro Gly Ala Val Ala His Ala Cys Asn Pro Ser Thr Leu
135 305 310 315 320
137 Gly Gly Arg Gly Gly Trp Ile Met Arg Ser Gly Asp Arg Asp His Pro

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145 <211> LENGTH: 1040
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152 ctggggatttc ccgttggccc aaggattcag atgctcctct ttgggctctt ctccctgttc 180
153 tacgtcttca ccctgctggg gaacgggacc atactggggc tcactctact ggactccaga 240
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155 tgcaacacgg tgccccggat gctggtgaac ctctgcatc cagccaagcc catctccttt 360
156 gcgggcccga tgatgcagac ctttctgttt tccacttttg ctgtcacaga atgtctcctc 420
157 ctggtggtga tgtcctatga tctgtacgtg gccatctgcc acccctccg atatttggcc 480
158 atcatgacct ggagagtctg catcacctc gcggtgactt cctggaccac tggagtcctt 540
159 ttatccttga ttcattctgt gttacttcta cctttaccct tctgtaggcc ccagaaaatt 600
160 tatcactttt tttgtgaaat cttggctgtt ctcaaacttg cctgtgcaga taccacatc 660
161 aatgagaaca tggctcttggc cggagcaatt tctgggctgg tgggaccctt gtccacaatt 720
162 gtagtttcat atatgtgcat cctctgtgct atccttcaga tccaatcaag ggaagttcag 780
163 aggaaagcct tccgcacctg cttctcccac ctctgtgtga ttggactcgt ttatggcaca 840
164 gccattatca tgtatgttgg acccagatat gggaacccca aggagcagaa gaaatatctc 900
165 ctgctgtttc acagcctctt taatcccatg ctcaatcccc ttatctgtag tcttaggaac 960
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180                               20                               25                               30
182 Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile
183                               35                               40                               45
185 Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr Phe Phe Leu Ser His
186   50                               55                               60
188 Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn Thr Val Pro Arg Met
189   65                               70                               75                               80
191 Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Arg
192                               85                               90                               95
194 Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala Val Thr Glu Cys Leu
195                               100                              105                              110
197 Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys His Pro
198                               115                              120                              125
200 Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val Cys Ile Thr Leu Ala
201   130                              135                              140
203 Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser Leu Ile His Leu Val

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206 Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln Lys Ile Tyr His Phe
207                      165                      170                      175
209 Phe Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Thr His
210                      180                      185                      190
212 Ile Asn Glu Asn Met Val Leu Ala Gly Ala Ile Ser Gly Leu Val Gly
213                      195                      200                      205
215 Pro Leu Ser Thr Ile Val Val Ser Tyr Met Cys Ile Leu Cys Ala Ile
216                      210                      215                      220
218 Leu Gln Ile Gln Ser Arg Glu Val Gln Arg Lys Ala Phe Arg Thr Cys
219 225                      230                      235                      240
221 Phe Ser His Leu Cys Val Ile Gly Leu Val Tyr Gly Thr Ala Ile Ile
222                      245                      250                      255
224 Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys Glu Gln Lys Lys Tyr
225                      260                      265                      270
227 Leu Leu Leu Phe His Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile
228                      275                      280                      285
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231                      290                      295                      300
233 Gly Val Glu Arg Ala Leu
234 305                      310
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245 acttgacaat cctggtggcc aatgtgacca tcattggcgt tattcgcttc agctggactc 180
246 tccacactcc catgtatggc tttctattca tcctttcatt ttctgagtcc tgctacactt 240
247 ttgtcatcat ccctcagctg ctggtccacc tgctctcaga caccaagacc atctccttca 300
248 tggcctgtgc caccagctg ttctttttcc ttggctttgc ttgcaccaac tgctcctca 360
249 ttgctgtgat gggatatgat cgctatgtag caatttgtca ccctctgagg tacacactca 420
250 tcataaaciaa aaggctgggg ttggagttga tttctctctc aggagccaca ggtttcttta 480
251 ttgctttggt ggccaccaac ctcatattgt acatgcgttt ttgtggcccc aacagggtta 540
252 accactattht ctgtgacatg gcacctgtta tcaagtttagc ctgcaactgac acccatgtga 600
253 aagagctggc tttatttagc ctacagcatcc tggttaattat ggtgcctttt ctgttaattc 660
254 tcataatcta tggtttcata gttacacca tcctgaagat cccctcagct gagggcaaga 720
255 aggcctttgt cacctgtgcc tcacatctca ctgtggtctt tgtccactat ggctgtgcct 780
256 ctatcatcta tctgcggccc aagtccaagt ctgcctcaga caaggatcag ttggtggcag 840
257 tgacctacac agtggttact cccttactta atcctcttgt ctacagtctg aggaacaaag 900
258 aggtaaaaaac tgcattgaaa agagttcttg gaatgcctgt ggcaaccaag atgagctaac 960
259 aaaaaataat aataaaatta actaggatag tcacagaaga aatcaaaggc ataaaaattht 1020
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265 <211> LENGTH: 314
266 <212> TYPE: PRT
267 <213> ORGANISM: Homo sapiens

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/898,586

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TIME: 12:51:19

Input Set : A:\Cural381.app

Output Set: N:\CRF3\09132001\I898586.raw

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274       20       25       30
276 Leu Leu Leu Tyr Leu Thr Ile Leu Val Ala Asn Val Thr Ile Met Ala
277       35       40       45
279 Val Ile Arg Phe Ser Trp Thr Leu His Thr Pro Met Tyr Gly Phe Leu
280       50       55       60
282 Phe Ile Leu Ser Phe Ser Glu Ser Cys Tyr Thr Phe Val Ile Ile Pro
283  65       70       75       80
285 Gln Leu Leu Val His Leu Leu Ser Asp Thr Lys Thr Ile Ser Phe Met
286       85       90       95
288 Ala Cys Ala Thr Gln Leu Phe Phe Phe Leu Gly Phe Ala Cys Thr Asn
289       100      105      110
291 Cys Leu Leu Ile Ala Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys
292       115      120      125
294 His Pro Leu Arg Tyr Thr Leu Ile Ile Asn Lys Arg Leu Gly Leu Glu
295       130      135      140
297 Leu Ile Ser Leu Ser Gly Ala Thr Gly Phe Phe Ile Ala Leu Val Ala
298 145       150       155       160
300 Thr Asn Leu Ile Cys Asp Met Arg Phe Cys Gly Pro Asn Arg Val Asn
301       165      170      175
303 His Tyr Phe Cys Asp Met Ala Pro Val Ile Lys Leu Ala Cys Thr Asp
304       180      185      190
306 Thr His Val Lys Glu Leu Ala Leu Phe Ser Leu Ser Ile Leu Val Ile
307       195      200      205
309 Met Val Pro Phe Leu Leu Ile Leu Ile Ser Tyr Gly Phe Ile Val Asn
310       210      215      220
312 Thr Ile Leu Lys Ile Pro Ser Ala Glu Gly Lys Lys Ala Phe Val Thr
313 225       230       235       240
315 Cys Ala Ser His Leu Thr Val Val Phe Val His Tyr Gly Cys Ala Ser
316       245      250      255
318 Ile Ile Tyr Leu Arg Pro Lys Ser Lys Ser Ala Ser Asp Lys Asp Gln
319       260      265      270
321 Leu Val Ala Val Thr Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Leu
322       275      280      285
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328 305       310
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339 acttgacaat cctggtggcc aatgtgacca tcatggccgt tattcgcttc agctgggactc 180

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/898,586

DATE: 09/13/2001

TIME: 12:51:20

Input Set : A:\Cura1381.app

Output Set: N:\CRF3\09132001\I898586.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:679 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14

L:1642 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35

L:1645 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35

L:2209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49

L:2212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49

L:2749 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63

L:2752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63